

217 #10



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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/758,017A

DATE: 02/14/2002

TIME: 10:10:39

Input Set : A:\U0132093.app

Output Set: N:\CRF3\02142002\I758017A.raw

3 <110> APPLICANT: Lanes, Olav
 4 Willasen, Nils Peder
 5 Guddal, Per Henrik
 6 Gjellesvik, Dag Rune
 8 <120> TITLE OF INVENTION: Cod uracil-DNA glycosylase, gene coding therefore,
 9 recombinant DNA containing said gene or operative parts
 10 thereof, a method for preparing said protein and the
 11 use of said protein or said operative pa
 13 <130> FILE REFERENCE: U013209-3
 15 <140> CURRENT APPLICATION NUMBER: 09/758,017A
 16 <141> CURRENT FILING DATE: 2001-01-10
 18 <150> PRIOR APPLICATION NUMBER: 2000 5428
 19 <151> PRIOR FILING DATE: 2000-10-27
 21 <150> PRIOR APPLICATION NUMBER: 2000 0163
 22 <151> PRIOR FILING DATE: 2000-01-12
 24 <160> NUMBER OF SEQ ID NOS: 19
 26 <170> SOFTWARE: PatentIn Ver. 2.0
 28 <210> SEQ ID NO: 1
 29 <211> LENGTH: 1283
 30 <212> TYPE: DNA
 31 <213> ORGANISM: Gadus morhua
 33 <220> FEATURE:
 34 <221> NAME/KEY: CDS
 35 <222> LOCATION: (18)..(920)
 37 <400> SEQUENCE: 1
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 39 Met Leu Phe Lys Leu Gly Leu Cys Gln Arg Cys
 40 1 5 10
 42 ata tca tca aat cgg gtg tta cca ggt tta cta att ccc caa act tta 98
 43 Ile Ser Ser Asn Arg Val Leu Pro Gly Leu Leu Ile Pro Gln Thr Leu
 44 15 20 25
 46 tgt ttt tct aaa tta atg aag ata acg ccg aag aaa ctg agg tcc tca 146
 47 Cys Phe Ser Lys Leu Met Lys Ile Thr Pro Lys Lys Leu Arg Ser Ser
 48 30 35 40
 50 aat gtg gaa caa aag acg tca tcg cca cag ctt tca gtg gag cag ctg 194
 51 Asn Val Glu Gln Lys Thr Ser Ser Pro Gln Leu Ser Val Glu Gln Leu
 52 45 50 55
 54 gaa aga atg gcc aaa aat aag aaa gca gcg ctt gac aag att aga gca 242
 55 Glu Arg Met Ala Lys Asn Lys Lys Ala Ala Leu Asp Lys Ile Arg Ala
 56 60 65 70 75
 58 aaa gca acg cct gca ggt ttc gga gag act tgg aga aga gag ctg gct 290
 59 Lys Ala Thr Pro Ala Gly Phe Gly Glu Thr Trp Arg Arg Glu Leu Ala
 60 80 85 90

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62	gca gag ttt gaa aag cca tac ttc aaa caa ttg atg tcc ttt gta gct	338
63	Ala Glu Phe Glu Lys Pro Tyr Phe Lys Gln Leu Met Ser Phe Val Ala	
64	95 100 105	
66	gat gag agg agc cgt cac acc gtc tac cca ccg gct gat caa gtg tac	386
67	Asp Glu Arg Ser Arg His Thr Val Tyr Pro Pro Ala Asp Gln Val Tyr	
68	110 115 120	
70	agt tcg aca gag atg tgt gac att caa gat gtg aaa gta gtg att cta	434
71	Ser Ser Thr Glu Met Cys Asp Ile Gln Asp Val Lys Val Val Ile Leu	
72	125 130 135	
74	ggc cag gac cct tac cac ggt ccc aac caa gca cat gga ctc tgt ttc	482
75	Gly Gln Asp Pro Tyr His Gly Pro Asn Gln Ala His Gly Leu Cys Phe	
76	140 145 150 155	
78	agt gtg caa aag cca gtt ccc cct ccc agt ctc gtg aac ata tac	530
79	Ser Val Gln Lys Pro Val Pro Pro Pro Ser Leu Val Asn Ile Tyr	
80	160 165 170	
82	aaa gaa ttg tgt acc gac att gat ggc ttc aag cat cct gga cat gga	578
83	Lys Glu Leu Cys Thr Asp Ile Asp Gly Phe Lys His Pro Gly His Gly	
84	175 180 185	
86	gat cta agc gga tgg gca aaa caa ggg gtg ctg ctg ctt aac gcg gtg	626
87	Asp Leu Ser Gly Trp Ala Lys Gln Gly Val Leu Leu Leu Asn Ala Val	
88	190 195 200	
90	ctg acc gtg cgg gcc cat cag gcc aac tcc cac aag gac aga ggc tgg	674
91	Leu Thr Val Arg Ala His Gln Ala Asn Ser His Lys Asp Arg Gly Trp	
92	205 210 215	
94	gag acc ttc acc gac gct gtg atc aag tgg ctg agc gtc aac cgg gaa	722
95	Glu Thr Phe Thr Asp Ala Val Ile Lys Trp Leu Ser Val Asn Arg Glu	
96	220 225 230 235	
98	gga gtc gtt ttc ctg ttg ggc tca tac gcc cat aag aag gga gcg	770
99	Gly Val Val Phe Leu Leu Trp Gly Ser Tyr Ala His Lys Lys Gly Ala	
100	240 245 250	
102	acc atc gac agg aaa cgt cac cat gtc ttg caa gct gtt cat cca tct	818
103	Thr Ile Asp Arg Lys Arg His His Val Leu Gln Ala Val His Pro Ser	
104	255 260 265	
106	cct ttg tct gct cat cgt ggg ttc ctt ggt tgt aag cac ttc tcc aag	866
107	Pro Leu Ser Ala His Arg Gly Phe Leu Gly Cys Lys His Phe Ser Lys	
108	270 275 280	
110	gct aac ggg ctg ctg aaa cta tct ggg acg gag cct ata aac tgg aga	914
111	Ala Asn Gly Leu Leu Lys Leu Ser Gly Thr Glu Pro Ile Asn Trp Arg	
112	285 290 295	
114	gca ctc taactcttta tgctgcctta tactgttaac tgtttaaga tgaacatcac	970
115	Ala Leu	
116	300	
118	actatatttt ctacagcttt tccaaagtca aaccaatcta taagctttca tttgtctttt	1030
120	ggaatgatgc tgcttttgtt cggtttttaga tactaaaac actttaccac tctgccatgt	1090
122	tgactcatgt tcagtcataa taactttcac aacttgaaca aaaatgttat tttataattg	1150
124	attatattct gtacattaaa gattgtttt ttcccaggct gtttcatagg tactaggata	1210
126	ttaaactgtt attaacctat ttccatgt gtcaactgct taagtttta tgcagaaata	1270
128	aattatataat tta	1283
131	<210> SEQ ID NO: 2	

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132 <211> LENGTH: 301
 133 <212> TYPE: PRT
 134 <213> ORGANISM: Gadus morhua
 136 <400> SEQUENCE: 2
 137 Met Leu Phe Lys Leu Gly Leu Cys Gln Arg Cys Ile Ser Ser Asn Arg
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 140 Val Leu Pro Gly Leu Leu Ile Pro Gln Thr Leu Cys Phe Ser Lys Leu
 141 20 25 30
 143 Met Lys Ile Thr Pro Lys Lys Leu Arg Ser Ser Asn Val Glu Gln Lys
 144 35 40 45
 146 Thr Ser Ser Pro Gln Leu Ser Val Glu Gln Leu Glu Arg Met Ala Lys
 147 50 55 60
 149 Asn Lys Lys Ala Ala Leu Asp Lys Ile Arg Ala Lys Ala Thr Pro Ala
 150 65 70 75 80
 152 Gly Phe Gly Glu Thr Trp Arg Arg Glu Leu Ala Ala Glu Phe Glu Lys
 153 85 90 95
 155 Pro Tyr Phe Lys Gln Leu Met Ser Phe Val Ala Asp Glu Arg Ser Arg
 156 100 105 110
 158 His Thr Val Tyr Pro Pro Ala Asp Gln Val Tyr Ser Ser Thr Glu Met
 159 115 120 125
 161 Cys Asp Ile Gln Asp Val Lys Val Val Ile Leu Gly Gln Asp Pro Tyr
 162 130 135 140
 164 His Gly Pro Asn Gln Ala His Gly Leu Cys Phe Ser Val Gln Lys Pro
 165 145 150 155 160
 167 Val Pro Pro Pro Pro Ser Leu Val Asn Ile Tyr Lys Glu Leu Cys Thr
 168 165 170 175
 170 Asp Ile Asp Gly Phe Lys His Pro Gly His Gly Asp Leu Ser Gly Trp
 171 180 185 190
 173 Ala Lys Gln Gly Val Leu Leu Leu Asn Ala Val Leu Thr Val Arg Ala
 174 195 200 205
 176 His Gln Ala Asn Ser His Lys Asp Arg Gly Trp Glu Thr Phe Thr Asp
 177 210 215 220
 179 Ala Val Ile Lys Trp Leu Ser Val Asn Arg Glu Gly Val Val Phe Leu
 180 225 230 235 240
 182 Leu Trp Gly Ser Tyr Ala His Lys Lys Gly Ala Thr Ile Asp Arg Lys
 183 245 250 255
 185 Arg His His Val Leu Gln Ala Val His Pro Ser Pro Leu Ser Ala His
 186 260 265 270
 188 Arg Gly Phe Leu Gly Cys Lys His Phe Ser Lys Ala Asn Gly Leu Leu
 189 275 280 285
 191 Lys Leu Ser Gly Thr Glu Pro Ile Asn Trp Arg Ala Leu
 192 290 295 300
 195 <210> SEQ ID NO: 3
 196 <211> LENGTH: 1355
 197 <212> TYPE: DNA
 198 <213> ORGANISM: Gadus morhua
 200 <220> FEATURE:
 201 <221> NAME/KEY: CDS
 202 <222> LOCATION: (90)..(992)

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204 <400> SEQUENCE: 3
 205 gatggtttag gaggatagta cttagacact ggttagcgaa ggggaaaacg gagttattgt 60
 207 gcatatcggtt ttagccctac gttaaaaaa atg att ggt caa cag cat atc aac 113
 208 Met Ile Gly Gln Gln His Ile Asn
 209 1 5
 211 tct ttc ttc tca cca gtt tca aaa aag aga gtt tca aag gaa tta ggt 161
 212 Ser Phe Phe Ser Pro Val Ser Lys Lys Arg Val Ser Lys Glu Leu Gly
 213 10 15 20
 215 aaa acc gaa aag cat gcc gaa gaa gtt cag ata acg ccg aag aaa ctg 209
 216 Lys Thr Glu Lys His Ala Glu Glu Val Gln Ile Thr Pro Lys Lys Leu
 217 25 30 35 40
 219 agg tcc tca aat gtg gaa caa aag acg tca tcg cca cag ctt tca gtg 257
 220 Arg Ser Ser Asn Val Glu Gln Lys Thr Ser Ser Pro Gln Leu Ser Val
 221 45 50 55
 223 gag cag ctg gaa aga atg gcc aaa aat aag aaa gca gcg ctt gac aag 305
 224 Glu Gln Leu Glu Arg Met Ala Lys Asn Lys Lys Ala Ala Leu Asp Lys
 225 60 65 70
 227 att aga gca aaa gca acg cct gca ggt ttc gga gag act tgg aga aga 353
 228 Ile Arg Ala Lys Ala Thr Pro Ala Gly Phe Gly Glu Thr Trp Arg Arg
 229 75 80 85
 231 gag ctg gct gca gag ttt gaa aag cca tac ttc aaa caa ttg atg tcc 401
 232 Glu Leu Ala Ala Glu Phe Glu Lys Pro Tyr Phe Lys Gln Leu Met Ser
 233 90 95 100
 235 ttt gta gct gat gag agg agc cgt cac acc gtc tac cca ccg gct gat 449
 236 Phe Val Ala Asp Glu Arg Ser Arg His Thr Val Tyr Pro Pro Ala Asp
 237 105 110 115 120
 239 caa gtg tac agt tgg aca gag atg tgt gac att caa gat gtg aaa gta 497
 240 Gln Val Tyr Ser Trp Thr Glu Met Cys Asp Ile Gln Asp Val Lys Val
 241 125 130 135
 243 gtg att cta ggc cag gac cct tac cac ggt ccc aac caa gca cat gga 545
 244 Val Ile Leu Gly Gln Asp Pro Tyr His Gly Pro Asn Gln Ala His Gly
 245 140 145 150
 247 ctc tgt ttc agt gtg caa aag cca gtt ccc cct ccc ccc agt ctc gtg 593
 248 Leu Cys Phe Ser Val Gln Lys Pro Val Pro Pro Pro Ser Leu Val
 249 155 160 165
 251 aac ata tac aaa gaa ttg tgt acc gac att gat ggc ttc aag cat cct 641
 252 Asn Ile Tyr Lys Glu Leu Cys Thr Asp Ile Asp Gly Phe Lys His Pro
 253 170 175 180
 255 gga cat gga gat cta agc gga tgg gca aac aag ggg tgc tgc tgc tta 689
 256 Gly His Gly Asp Leu Ser Gly Trp Ala Asn Lys Gly Cys Cys Cys Leu
 257 185 190 195 200
 259 acg cgc tgc ctg acc gtg cgg gcc cat cag gcc aac tcc cac aag gac 737
 260 Thr Arg Cys Leu Thr Val Arg Ala His Gln Ala Asn Ser His Lys Asp
 261 205 210 215
 263 aga ggc tgg gag acc tcc acc gac gct gtg atc aag tgg ctg agc gtc 785
 264 Arg Gly Trp Glu Thr Ser Thr Asp Ala Val Ile Lys Trp Leu Ser Val
 265 220 225 230
 267 aac cgg gaa gga gtg gtt ttc ctg ttc tgg ggc tca tac gcc cat aag 833
 268 Asn Arg Glu Gly Val Val Phe Leu Phe Trp Gly Ser Tyr Ala His Lys

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269	235	240	245	
271	aag gga gcg acc atc gac agg aaa cgt cac cat gtc ttg caa gct ctt			881
272	Lys Gly Ala Thr Ile Asp Arg Lys Arg His His Val Leu Gln Ala Leu			
273	250	255	260	
275	cat cca tct cct ttg tct gct cat cgt ggg ttc ctt ggt tgt aag cac			929
276	His Pro Ser Pro Leu Ser Ala His Arg Gly Phe Leu Gly Cys Lys His			
277	265	270	275	280
279	ttc tcc aag gct aac ggg ctg ctg aaa cta tct ggg acg gag cct ata			977
280	Phe Ser Lys Ala Asn Gly Leu Leu Lys Leu Ser Gly Thr Glu Pro Ile			
281	285	290	295	
283	aac tgg aga gca ctc taactcttta tgctgcctta tactgttaac tgtttaaga			1032
284	Asn Trp Arg Ala Leu			
285	300			
287	tgaacatcac actatatttt ctacagcttt tccaaagttca aaccaatcta taagctttca			1092
289	tttgcctttt ggaatgatgc tgcttttgt cggttttaga tacttaaaac actttaccac			1152
291	tctgccatgt tgactcatgt tcagtcaata taactttcac aacttgaaca aaaatgttat			1212
293	tttataattt attatattct gtacattaaa gattgtttt ttcccaggct gttcataagg			1272
295	tactaggata tttaactgtt attaacctat ttccatgtat gtcaactgct taagtttta			1332
297	tgcagaaata aattatataat tta			1355
300	<210> SEQ ID NO: 4			
301	<211> LENGTH: 301			
302	<212> TYPE: PRT			
303	<213> ORGANISM: Gadus morhua			
305	<400> SEQUENCE: 4			
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307	1	5	10	15
309	Lys Arg Val Ser Lys Glu Leu Gly Lys Thr Glu Lys His Ala Glu Glu			
310	20	25	30	
312	Val Gln Ile Thr Pro Lys Lys Leu Arg Ser Ser Asn Val Glu Gln Lys			
313	35	40	45	
315	Thr Ser Ser Pro Gln Leu Ser Val Glu Gln Leu Glu Arg Met Ala Lys			
316	50	55	60	
318	Asn Lys Lys Ala Ala Leu Asp Lys Ile Arg Ala Lys Ala Thr Pro Ala			
319	65	70	75	80
321	Gly Phe Gly Glu Thr Trp Arg Arg Glu Leu Ala Ala Glu Phe Glu Lys			
322	85	90	95	
324	Pro Tyr Phe Lys Gln Leu Met Ser Phe Val Ala Asp Glu Arg Ser Arg			
325	100	105	110	
327	His Thr Val Tyr Pro Pro Ala Asp Gln Val Tyr Ser Trp Thr Glu Met			
328	115	120	125	
330	Cys Asp Ile Gln Asp Val Lys Val Val Ile Leu Gly Gln Asp Pro Tyr			
331	130	135	140	
333	His Gly Pro Asn Gln Ala His Gly Leu Cys Phe Ser Val Gln Lys Pro			
334	145	150	155	160
336	Val Pro Pro Pro Ser Leu Val Asn Ile Tyr Lys Glu Leu Cys Thr			
337	165	170	175	
339	Asp Ile Asp Gly Phe Lys His Pro Gly His Gly Asp Leu Ser Gly Trp			
340	180	185	190	
342	Ala Asn Lys Gly Cys Cys Cys Leu Thr Arg Cys Leu Thr Val Arg Ala			

VERIFICATION SUMMARY

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